

LOCUS AF089816 **1765 bp** **mRNA** **linear** **PRI** 24-OCT-1998
DEFINITION Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.
ACCESSION AF089816
VERSION AF089816.1 GI:3789933
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1765)
AUTHORS De Vries,L., Lou,X., Zhao,G., Zheng,B. and Farquhar,M.G.
TITLE GIPC, a PDZ domain containing protein, interacts specifically with
the C terminus of RGS-GAIP
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12340-12345 (1998)
MEDLINE 98445373
PUBMED 9770488
REFERENCE 2 (bases 1 to 1765)
AUTHORS De Vries,L., Lou,X., Zhao,G., Zheng,B. and Farquhar,M.G.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1998) CMM, UCSD, 9500 Gilman Drive, La Jolla, CA
92093, USA
FEATURES Location/Qualifiers
source 1. .1765
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="GC"
/tissue_type="pituitary"
/note="growth hormone secreting cells"
CDS 88. .1089
/codon_start=1
/product="RGS-GAIP interacting protein GIPC"
/protein_id="AAC67548.1"
/db_xref="GI:3789934"
/translation="MPLGLGRRKKAPPLVENEEAEPGRGGLGVGEPGPLGGGGSGGPQ
MGLPPPPPALARPRLVFHTQLAHGSPTGRIEGFTNVKELYGKIAEAFRLPTAEVMFCTL
NTHKVDMKDQLGGQIGLEDFIFAHVKGQRKEVEVFKSEDALGLTITDNGAGYAFIKRI
KEGSVIDHIHLISVGDMIEAINQSQSLLGCRHYEVARLLKELPRGRTFTLKLTEPRKAF
DMISQRSAGGRPGSGPQLTGRGTLRLRSRGPATVEDLPSAFEKAIKEKVDDLLESYM
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misc_feature 460. .762
/note="encodes PDZ domain"
misc_feature 877. .1047
/note="encodes ACP domain"
BASE COUNT 332 a 561 c 568 g 304 t
ORIGIN

Alignment Scores:

Pred. No.:	2.08e-102	Length:	1765
Score:	1713.00	Matches:	330
Percent Similarity:	99.10%	Conservative:	0
Best Local Similarity:	99.10%	Mismatches:	3
Query Match:	99.59%	Indels:	0
DB:	9	Gaps:	0

US-10-013-056-2 (1-333) x AF089816 (1-1765)

Qy	1	MetProLeuGlyLeuGlyArgArgLysLysAlaProProLeuValGluAsnGluGluAla	20
Db	88	ATGCCGCTGGACTGGGCAGCCGGAAAAAGGCGCCCCCTCTAGTGGAAAATGAGGAGGCT	147
Qy	21	GluProGlyArgGlyGlyLeuGlyValGlyGluProGlyProLeuGlyGlyGlySer	40
Db	148	GAGCCAGGCCGTGGAGGGCTGGCGTGGGGAGCCAGGGCCTTGGCCGGAGGTGGTCG	207
Qy	41	Gly***ProGlnMetGly*****ProProProProAlaLeuArgProArgLeuValPhe	60
Db	208	GGGGGCCCAAAATGGGCTTGCCCCCCCCTCCCCAGCCCTGCGGCCCGCCTGTGTTG	267
Qy	61	HisThrGlnLeuAlaHisGlySerProThrGlyArgIleGluGlyPheThrAsnValLys	80
Db	268	CACACCCAGCTGGCCATGGCAGTCCCCTGGCCGCATCGAGGGGTTCACCAACGTCAAG	327
Qy	81	GluLeuTyrGlyLysIleAlaGluAlaPheArgLeuProThrAlaGluValMetPheCys	100
Db	328	GAGCTGTATGGCAAGATTGCCGAGGCCTTCCGCCTGCCACTGCCGAGGTGATGTTTGC	387
Qy	101	ThrLeuAsnThrHisLysValAspMetAspLysLeuLeuGlyGlyGlnIleGlyLeuGlu	120
Db	388	ACCCTGAACACCCACAAAGTGGACATGGACAAGCTCCTGGGGGCCAAATGGGCTGGAG	447
Qy	121	AspPheIlePheAlaHisValLysGlyGlnArgLysGluValGluValPheLysSerGlu	140
Db	448	GACTTCATCTCGCCCACGTGAAGGGCAGCGCAAGGAGGTGGAGGTGTTCAAGTCGGAG	507
Qy	141	AspAlaLeuGlyLeuThrIleThrAspAsnGlyAlaGlyTyrAlaPheIleLysArgIle	160
Db	508	GATGCACTCGGGCTCACCATCACGGACAACGGGGCTGGCTACGCCCTCATCAAGCGCATC	567
Qy	161	LysGluGlySerValIleAspHisIleHisLeuIleSerValGlyAspMetIleGluAla	180
Db	568	AAGGAGGGCAGCGTGATCGACCACATCCACCTCATCAGCGTGGCGACATGATCGAGGCC	627
Qy	181	IleAsnGlyGlnSerLeuLeuGlyCysArgHisTyrGluValAlaArgLeuLeuLysGlu	200
Db	628	ATTAACGGGCAGAGCCTGCTGGCTGCCGGCACTACGAAGTGGCCGGCTGCTCAAGGAA	687
Qy	201	LeuProArgGlyArgThrPheThrLeuLysLeuThrGluProArgLysAlaPheAspMet	220
Db	688	CTGCCCGAGGCCGTACCTCACGCTGAAGCTCACGGAGCCTCGCAAGGCCCTCGACATG	747
Qy	221	IleSerGlnArgSerAlaGlyGlyArgProGlySerGlyProGlnLeuGlyThrGlyArg	240
Db	748	ATCAGCCAGCGTTCAGCGGGTGGCCGCCCTGGCTCTGGCCCACAACTGGGCACTGGCCGA	807
Qy	241	GlyThrLeuArgLeuArgSerArgGlyProAlaThrValGluAspLeuProSerAlaPhe	260
Db	808	GGGACCCCTGCGGCTCCGATCCCAGGGGCCACGGTGGAGGATCTGCCCTCGCCTT	867
Qy	261	GluGluLysAlaIleGluLysValAspAspLeuLeuGluSerTyrMetGlyIleArgAsp	280
Db	868	GAAGAGAAGGCCATTGAGAAGGTGGATGACCTGCTGGAGAGTTACATGGGTATCAGGGAC	927
Qy	281	ThrGluLeuAlaAlaThrMetValGluLeuGlyLysAspLysArgAsnProAspGluLeu	300

Db 928 ACGGAGCTGGCGGCCACCATGGTGGAGCTGGGAAAGGACAAAAGGAACCCGGATGAGCTG 987
Qy 301 AlaGluAlaLeuAspGluArgLeuGlyAspPheAlaPheProAspGluPheValPheAsp 320
Db 988 GCCGAGGCCCTGGACGAACGGCTGGGTGACTTGCCTCCCTGACGAGTTCGTCTTGAC 1047
Qy 321 ValTrpGlyAlaIleGlyAspAlaLysValGlyArgTyr 333
Db 1048 GTCTGGGGCGCCATTGGGGACGCCAAGGTCGGCCGCTAC 1086